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Assessing the conservation value of waterbodies: the example of the Loire floodplain (France)

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Abstract
In recent decades, two of the main management tools used to stem biodiversity erosion have been biodiversity monitoring and the conservation of natural areas. However, socio-economic pressure means that it is not usually possible to preserve the entire landscape, and so the rational prioritisation of sites has become a crucial issue. In this context, and because floodplains are one of the most threatened ecosystems, we propose a statistical strategy for evaluating conservation value, and used it to prioritise 46 waterbodies in the Loire floodplain (France). We began by determining a synthetic conservation index of fish communities (Q) for each waterbody. This synthetic index includes a conservation status index, an origin index, a rarity index and a richness index. We divided the waterbodies into 6 clusters with distinct structures of the basic indices. One of these clusters, with high Q median value, indicated that 4 waterbodies are important for fish biodiversity conservation. Conversely, two clusters with low Q median values included 11 waterbodies where restoration is called for. The results picked out high connectivity levels and low abundance of aquatic vegetation as the two main environmental characteristics of waterbodies with high conservation value. In addition, assessing the biodiversity and conservation value of territories using our multi-index approach plus an a posteriori hierarchical classification methodology reveals two major interests: (i) a possible geographical extension and (ii) a multi-taxa adaptation.

Keywords Hierarchical organization – Floodplain – Waterbody – Conservation status – Rarity index – Origin index – Management

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Introduction

The current biodiversity loss due to global changes has been considered as heralding the dawn of a sixth extinction crisis (Thomas et al. *2004*). Some of the most threatened ecosystems are freshwater habitats with their associated species (Dudgeon et al. *2006*). At the scale of the individual catchment area, river floodplains are usually described as centres of biological diversification (Naiman et al. *1993*) but, as a result of severe anthropological degradation worldwide, they are highly endangered (Tockner and

Stanford 2002).

Since the European Water Framework Directive came into force (Kallis and Butler 2001), the need to be able to select freshwater sites for conservation on the basis of their ecological status has become a central objective for conservation agencies. In addition, according to Chovanec et al. (2005), particular efforts have to be made to develop appropriate indices for monitoring inland water. Floodplain conservation and restoration management can be divided into two tasks corresponding to (i) catchment management covering a fairly large area around freshwater bodies (Saunders et al. 2002) and (ii) selective management resulting from site prioritisation (Bergerot et al. 2008). Because government agencies responsible for biodiversity conservation face spiralling costs and limited funding, socio-economic pressures make it impossible to conserve the entire landscape together with the associated biodiversity. Prioritising sites and developing indices that will make it possible to select the most important areas to conserve are required to achieve the necessary trade-off between sustainable conservation and a more business-oriented approach (Inamdar et al. 1999). One conservation approach involves setting up protected areas (Abell et al. 2007), selected on the basis of their conservation value. Consequently, a plethora of indices has been proposed for evaluating the conservation value of species assemblages and the territories associated with them. The diversity of these conservation indices is probably related to the variety of scales of investigation used or to the wide range of community attributes selected for consideration, such as conservation status (Fattorini 2006a), perturbation (Oberdorff et al. 2002), rarity (Kerr 1997), guilds (Aarts and Nienhuis 2003), umbrella species (Bried et al. 2007) etc. Nevertheless, as suggested by Fattorini (2006b) and applied by Bergerot et al. (2008) or Turak and Koop (2008), a multi-index approach to assess conservation value could provide a flexible and informative method of prioritising sites, and identifying territories that are important for biodiversity conservation or restoration.

Freshwater fish constitute an interesting model for studying floodplain ecological status due to their sensitivity to environment degradation (Schiemer 2000; Oberdorff et al. 2002). For this reason, previous studies of temperate floodplains have used the fish community to assess biological integrity (Amoros and Bornette 2002; Aarts and Nienhuis 2003; Lasne et al. 2007a). In this paper, our objectives were: (i) to evaluate the conservation value of various waterbodies in the Loire floodplain (France) by a multi-index approach, (ii) to devise a classification model to improve the caregorization of the conservation value of waterbodies and (iii) to explore the environmental factors that determine conservation value.

Materials and methods

The study area

The Loire River basin, located in Northwest France, drains a 117,000 km^2 catchment area and flows into the Atlantic Ocean. As flood discharges are virtually unregulated in most of the main river, the Loire (1012 km long), the IUCN considers it to be the “last wild large river in Europe” (http://www.uicn.org). Even though human activities have required the construction of levees and dams, the hydrological regime of the Loire is characterized by large seasonal variations in discharge volumes, with low flow levels in summer and high flow levels in winter. The floodplain is located in the downstream segment of the Loire, in the zone inhabited by bream (*Abramis brama*) (Lasne et al. 2007b). According to the typology formulated by Amoros et al. (1987), in the 130-km section studied here (Fig. 1) there is a wide diversity of waterbodies ranging from eupotamon (sidearms), to paleopotamon and temporary wetlands. As a result, the lateral floodplains are more or less connected to the Loire River itself. The limit of salt water intrusion into the main channel corresponds roughly to the downstream limit of our sampling area. From there on, the water is fresh and its salinity close to 0. In this part of the Loire River, the absence of barriers permits the free downstream-upstream migration of fish (Lasne et al. 2008).

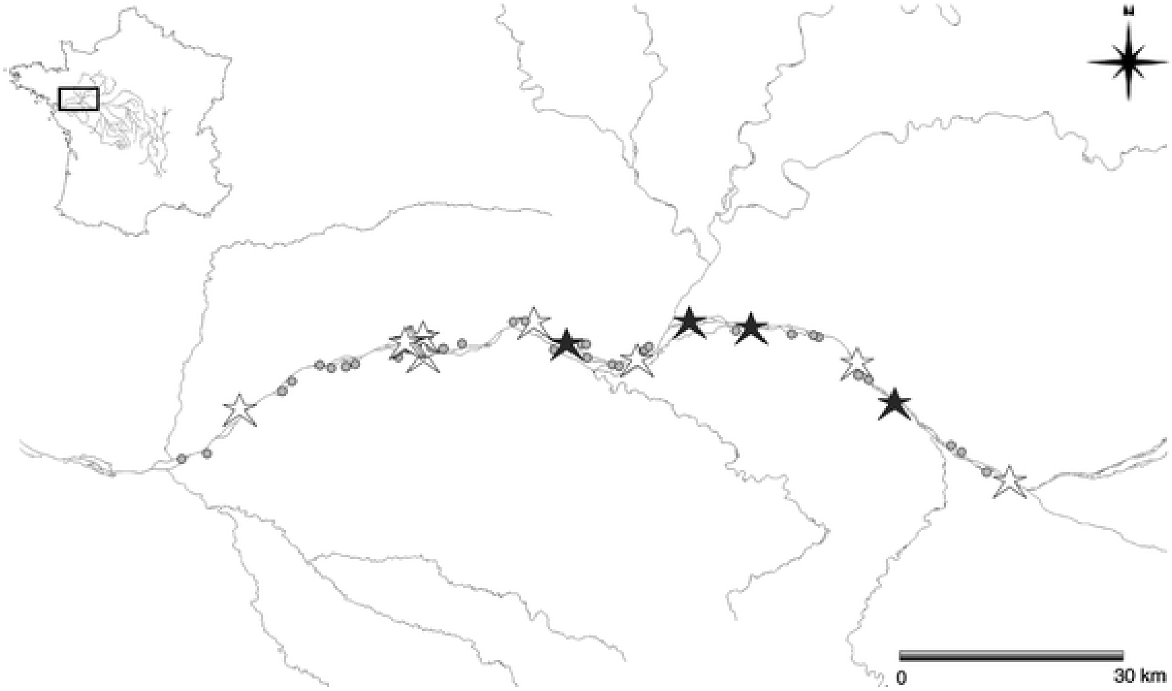

Fig. 1 Study sector. Locations of the 46 waterbodies sampled in the Loire basin river. The waterbodies that should be conserved are indicated by black stars, and those that should be restored are indicated by white stars

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Data collection

We sampled fish in June 2004 and June 2005 in 46 waterbodies (data used in Lasne et al. *2007a*). During the sampling campaigns, the flow was slow enough to allow considerable habitat heterogeneity in the floodplain (according to the ''telescoping model'' of Ward and Tockner *2001*). Indeed, prior to the time of year our sampling began (i.e. during the flood pulse), most of the waterbodies are interconnected, and fish are relatively free to move across the floodplain. At the onset of the dry phase (i.e. in May–June), habitat heterogeneity increases markedly, and fish settle in the various waterbodies on the basis of their individual species requirements for growth or reproduction. Consequently, an analysis fish distribution carried out in June should be particularly informative. Later in the dry period (August or September), some waterbodies may dry up dramatically (even completely), which could bias fish distribution by altering population densities.

We used the Point Abundance Sampling (PAS) electrofishing method described by Nelva et al. (*1979*) and Laffaille et al. (*2005*). This is a quick and cheap method that provides reproducible and quantitative samples, making it possible to carry out spatial comparisons between the sampling sites. In order to get a representative image of the structure of fish taxocoenoses, we performed 25–35 random PASs in the various microhabitats of each waterbody. Fish species were identified at each PAS, and presence–absence data were used in order to calculate the occurrence frequency of species within each waterbody (i.e. the frequency of PASs in which the species was detected) as an index of local species abundance. At the scale of the PAS (i.e. fish microhabitat), we measured or estimated the percentage of floating aquatic vegetation cover (water lilies and duckweed especially, scored from 0 to 100), the percentage of submerged vegetation in the water column (scored from 0 to 100), the substratum composition (presence of silt and pebbles), and the topography (by an index of the slope of the waterbed, which ranged from 0 for a flat waterbed to 5 for a steep waterbed). As recommended by Copp (*1989*), we used mean values of microhabitat variables to characterize the sites. At the waterbody and floodplain scale (i.e. fish mesohabitat), we extracted the distances to the saline limit (in km, ranging from −8.5 to 129, because two site were located downstream of the limit of salt water intrusion) by map analysis, and we evaluated the waterbody connectivity on the basis of previous studies (Lasne et al. *2007a*). Hydrological connectivity decreases from class 5 to class 0: 5 = sidearm connected at both ends during the sampling period; 4 = sidearm connected at the downstream end during the sampling period; 3 = sidearm not connected during the sampling period; 2 = abandoned sidearm regularly connected at the downstream end during winter flow; 1 = isolated waterbodies close to the main channel (<500 m) and connected during moderate winter flooding; 0 = isolated waterbodies some distance away from the main channel (>500 m).

Data analysis

Conservation and biodiversity indices

The biodiversity and/or conservation value of assemblages can be diversely assessed using different indices (Darwall and Vié 2005). In this study, we selected four basic indices to combine various facets of biodiversity and conservation value: the biodiversity conservation concern index (BCC), the origin index (OI), the rarity index (RI), and the richness index (Rich). We then summed these indices to construct an aggregative conservation index (*Q*) according to the method of Bergerot et al. (2008). The biodiversity conservation concern index, based on the conservation status weight for each species in a given community, is a modified version of the index constructed by Fattorini (2006a). The BCC index is calculated from

$$\mathrm{BCC} = \sum_{j=1}^{K} \frac{\alpha_j A_j}{S} - 1$$

where BCC is the biodiversity conservation concern index, K is the total number of species of the study, α_j the weight assigned to the jth species, A_j the presence (=1) or absence (=0) of jth species in the species assemblage, and S the total number of species in the species assemblage:

$$S = \sum_{j=1}^{K} A_j$$

For a given species, the conservation weights indicate the level of attention stipulated by conservation laws. We carried out the weight calculation (α) for each species according to the 2^n geometric series, where n is the sum of species protection value according to the European Directive "Fauna-Flora-Habitats" (directive 93/43/CEE, dated 21/5/1992), the Berne Convention (1979), and the UICN (International Union for the Conservation of Nature) Red List of Threatened Species (1994). We allocated a value of 0.5 to species included in the annexes II or IV of the Habitat Directive (and consequently a value of 1 for species included in both annexes), 1 for species in Annex III of the Berne Convention, and progressive values from 0.2 to 0.8 based on the IUCN status (0.2 for Lower Risk, 0.4 for VUlnerable, 0.6 for ENdangered, 0.8 for Critically Endangered respectively). The use of a geometric formula makes it possible for species with a low value to move quickly to a higher value, and consequently provides a better representation of increasing values in the final BCC. In contrast to Fattorini (2006a), we divided each BCC by the BBC_{max} in order to obtain a range of values from 0 (for a sampling site that did not include any protected species) to 1 (for a sampling site including protected species with highest value in the dataset). To make sure that the BCC index was not statistically influenced by the species protection lists and the number of lists used (i.e. to test the sensitivity of the discrimination method), we carried out Spearman correlation tests with a Holm-Bonferroni P value correction between all the BCCs arranged with two or three lists (r between 0.883 and 0.984, $P < 0.001$ in all pairwise correlations).

According to Kennard et al. (2005), the presence of alien species is a good indicator of biological change in rivers. We calculated the origin index (OI) as the ratio between the number of native species and the total number of species in a given waterbody. Thus, the closer the OI index is to 1, the higher the proportion of native species. Conversely, the closer the OI index is to 0, the lower the proportion of native species, and thus the weaker the integrity of a waterbody.

The rarity index (RI) measures the rarity of a fish assemblage based on a rarity weight assigned to each species. The rarity weights were carried out for each fish species as the inverse of the size of their geographic range (corresponding to $1/N_{pw,}$ with N_{pw} is the number of waterbodies in which the species occurs). Then, the waterbody values of RI were computed as the sum of the rarity weights of the fish assemblage (Kerr 1997; Fattorini 2006b). Finally, we divided each IR by the IR_{max} in order to obtain values ranging from 0 to 1. This rarity index tended towards 1 when the sample consisted entirely of scarce species, and tended towards 0 when there were no scarce species in the sample.

Many studies have shown that species richness is related to ecological interest, and must be viewed as an important factor in conservation prioritisation (Heino 2002). We defined the richness index (Rich) as the ratio between the species richness of a given waterbody and the maximum waterbody richness identified. To permit comparisons with the other indices, Rich values ranged between 0 (a waterbody containing no species) and 1 (a waterbody with the maximum number of different species).

For each waterbody, we constructed the synthetic conservation value index (Q) by summing the BCC, OI, RI and Rich indices. This synthetic index ranged from 0 to 4: 0 for a site with low overall conservation value (i.e. with few species of conservation concern, low richness, few rare species and a lot of non-native species), to 4 for sites with a high assemblage conservation value (i.e. with many species of conservation concern, high richness, many rare species and few non-native species).

To make sure that these basic indices were statistically independent, we carried out Spearman correlation tests with a Holm-Bonferroni P value correction (r between −0.11 and +0.38, $P > 0.05$ in all pairwise correlations).

Site discrimination

Based on these independent basic indices, we ordinated the waterbodies using a self organizing map (SOM). This non-supervised artificial neural network (ANN) method makes it possible to analyse of complex data sets with non-linear relationships (Kohonen 2001). The SOM architecture includes two layers: an input layer with discriminating variables (input neurons), and an output layer corresponding to a two-dimensional cell grid (output neurons). At the end of the procedure, the SOM algorithm assigns waterbodies with similar basic conservation indices to the same output neuron, or to the neighbouring neurons (see Kohonen 2001; Park et al. 2006 and Giraudel and Lek 2001 for details about the learning rules of such neural network). In this study, we used four input neurons (i.e. the four basic indices) to define the vectors of the input dataset (i.e. the waterbodies), and hexagonal cells organized on a map for the output layer. According to the building rules recommended by Vesanto and Alhoniemi (2000) and Kohonen (2001), we compiled a map with a 35-cell ([7 × 5] architecture). Finally, we used the virtual waterbody values resulting of trained SOMs in a clustering technique (Euclidean dissimilarity and UPGMA linkage) to group the SOM output neurons into meaningful clusters. In fact, to test the hypothesis for differences among group sites with respect to basic indices, we carried out a pairwise Multi-Response Permutation Procedure (MRPP) (Mielke et al. 1981) on the value of the output neurons (representing the virtual waterbodies) with a Holm-Bonferroni P value correction. The MRPP procedure evaluates the probability to observe a difference between the within-group agreement statistic (the agreement statistic A describes the within-group homogeneity compared to random expectation) and the observed intragroup average distances. In this study, we used the Euclidean distance and group size weighting to calculate mean within-group index distances. We carried out the MRPP procedure each time that a new group was created by the dendrogram. We defined the SOM dendrogram threshold subdivision as where the maximum number of statistically different clusters were obtained. Finally, the occurrence frequencies of each species, and the basic and synthetic indices in the different clusters identified were compared using Kruskall–Wallis tests and Dunn’s post-hoc test.

Environmental determinism of conservation value

In order to find out whether the basic and synthetic indices were related to environmental variables, we carried out a supervised artificial neural network (ANN). We predicted the BCC, OI, RI, Rich and *Q* indices with a backpropagation learning algorithm known as multilayer perceptron (MLP) using the 7 environmental variables. In our study, the MLP architecture comprised three layers: an input layer corresponding to the environmental variables (7 neurons), a hidden layer (the number of neurons fixed by calibration), and an output layer corresponding to the predicted indices for sites (46 neurons). The neurons in each layer are connected to all the neurons in the adjacent layers. These neurons transmit the signal they receive through these connections, which are assigned a weight value. Under the rules of this statistical model, weight corrections were implemented at each iteration following a stochastic gradient in order to minimise the mean square error between the computed output of the network and the desired output (for a detailed description of the learning rules of MLP see Lek et al. *1996*; Spitz and Lek *1999*). We fixed the optimal parameterisation (number of hidden neurons and number of iterations) as the trade-off between biases and variances. We used a leave-one-out cross-validation test to validate the accuracy of MLP model, and evaluated the performance of the MLP models. After the learning and validation process, we evaluated the contribution of each input variable to the output values using a sensitivity analysis based on the partial derivatives method (PaD) (Dimopoulos et al. *1995*), one the most useful methods for testing the sensitivity of independent variables (Gevrey et al. *2003*). The PaD method estimated the relative contributions of environmental variables as the square of partial derivate sum for each index. Because random values were assigned to the weights at the beginning of the training stage, the process was repeated 50 times per model in order to evaluate the stability of the contribution. Finally, to visualize the relationships between the indices and the two most strongly contributing variables, we displayed a non-parametric regression model, the Lowess smoothing plots (Trexler and Travis *1993*), which is known to be a reliable way to fit data tendencies, and to preserve the natural nonlinearity of the data.

To test the sensitivity of our statistical strategy, parallel analyses using only two protection lists for the BBC calculation index or a log-transformed richness index were performed with the entire modelling process (not shown in this study).

In the calculation process, the data were not transformed, because no assumptions about linearity, normality and homogeneity of variance are required for the ANN and MRPP methods. The ANN models were generated using Matlab® software language (Mathworks, Natick, MA, USA), and the other analyses and the map were performed using R statistical freeware.

Results

Floodplain fish diversity

We sampled a total of 16,000 individuals from the 46 waterbodies investigated for a total of 30 species (Table 1). We pooled *Abramis brama* and *Blicca bjoerkna* as "bream" because it is difficult to identify the species of the youngest individuals. The proportion of occupied sites (OS) varied considerably according to species. The most frequently occurring fish (OS > 75%) at the scale of the entire Loire floodplain were the pumpkinseed (*Lepomis gibbosus*), the European eel (*Anguilla anguilla*), the "bream" and the roach (*Rutilus rutilus*). Of the 30 species identified, 20 benefited from special conservation status, and 9 were non-native species (Table 1) (see Lasne et al. *2007a* for more details).

Table 1 Conservation status and classification of fish species caught in the 46 waterbodies of Loire floodplain in June 2004 and June 2005

Common name	Conservation status[a]			OS[b]	SOM clustering[c]						
	Origin	Conservation degree	BCC weight	(%)	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	K–W

Pumpkinseed	E	–	0	89	0.30	0.46	0.38	0.35	0.14	0.03	ns
European eel	N	–	0	85	0.19	0.50	0.37	0.31	0.03	0.04	ns
Breams	N	IUCN(LR)	0.2	83	0.17 a	0.19 a	0.14 a	0.07 ab	0.06 ab	0.00 b	*
Common roach	N	IUCN(LR)	0.2	83	0.38 a	0.32 a	0.36 a	0.11 b	0.09 b	0.00 c	***
Bitterling	N	H(II), B(III)	1.7	72	0.39 a	0.11 b	0.23 ab	0.11 b	0.00 c	0.00 c	***
European perch	N	IUCN(LR)	0.2	65	0.03 b	0.14 a	0.17 a	0.00 b	0.00 b	0.04 b	**
False harlequin	E	–	0	63	0.05	0.04	0.04	0.04	0.10	0.00	ns
Common bleak	N	IUCN(LR)	0.2	61	0.26 a	0.10 ab	0.08 ab	0.00 c	0.00 c	0.00 c	***
Northern pike	N	–	0	59	0.02	0.03	0.04	0.00	0.00	0.05	ns
Black bullhead	E	–	0	57	0.00	0.16	0.05	0.27	0.30	0.03	ns
Common chub	N	IUCN(LR)	0.2	54	0.29 a	0.06 b	0.06 b	0.00 b	0.00 b	0.00 b	**
Common gudgeon	N	IUCN(LR)	0.2	43	0.41 a	0.07 b	0.03 b	0.00 b	0.00 b	0.00 b	**
Common rudd	N	IUCN(LR)	0.2	41	0.00	0.00	0.00	0.02	0.00	0.02	ns
Tench	N	IUCN(LR)	0.2	35	0.00	0.04	0.00	0.00	0.00	0.00	ns
Pikeperch	E	IUCN(LR)	0.2	33	0.00	0.00	0.00	0.02	0.04	0.00	ns
Common barbel	N	H(V), IUCN (LR)	0.7	20	0.00 b	0.00 b	0.00 b	0.07 ab	0.13 a	0.00 b	***
Crucian carp	E	IUCN(LR)	0.2	15	0.00	0.00	0.00	0.00	0.00	0.00	ns
Common carp	E	–	0	15	0.00	0.00	0.00	0.00	0.00	0.00	ns
Ruffe	N	IUCN(LR)	0.2	13	0.03 a	0.00 b	0.00 b	0.00 b	0.00 b	0.00 b	*
Wels catfish	E	B(III), IUCN (LR)	1.2	13	0.00 b	0.03 a	0.00 b	0.00 b	0.00 b	0.00 b	*
Common dace	N	IUCN(LR)	0.2	11	0.12 a	0.00 b	0.00 b	0.00 b	0.00 b	0.00 b	***

Largemouth bass	E	–	0	7	0.00	0.00	0.00	0.00	0.00	0.00	ns
Sea lamprey	N	H(II), B(III), IUCN(LR)	1.9	7	0.00	0.00	0.00	0.00	0.00	0.00	ns
Mosquito fish	E	–	0	4	0.00	0.00	0.00	0.00	0.00	0.00	ns
Three-spined stickleback	N	IUCN(LR)	0.2	4	0.00	0.00	0.00	0.00	0.00	0.00	ns
Atlantic flounder	N	–	0	4	0.00	0.00	0.00	0.00	0.00	0.00	ns
Schneider	N	B(III), IUCN (LR)	1.2	2	0.00	0.00	0.00	0.00	0.00	0.00	ns
Common nase	N	B(III), IUCN (LR)	1.2	2	0.00	0.00	0.00	0.00	0.00	0.00	ns
Spined loach	N	H(II), B(III), IUCN(LR)	1.9	2	0.00	0.00	0.00	0.00	0.00	0.00	ns
Thin-lipped grey mullet	N	–	0	2	0.00	0.00	0.00	0.00	0.00	0.00	ns

[a]Origin is coded as N for native and E for non-native species (according to Keith and Allardi 2001 and Copp et al. 2005 definition). The inclusion of species in red-lists or other protection lists is indicated as follows: H(II) and H(V) indicate Annexes II and V of the Habitat Directive, respectively; B(III) indicates Annex III of the Berne Convention, IUCN(LC) = Lower Risk status in the IUCN classification)

[b]OS: Proportion of occupied sites ($N = 46$)

[c]Median of PAS occurrence frequencies for the SOM clusters. Differences among clusters were tested for each species by a Kruskall–Wallis test (K–W). Median values followed by the same letter are not statistically different ($\alpha = 0.05$) according to Dunn's post-hoc tests when Kruskall–Wallis tests were significant ($\alpha = 0.05$; *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$, *ns* not significant)

Waterbody clustering

The MRPP subdivision of clusters obtained using a SOM procedure identified six statistically different clusters (Fig. 2). The distribution of sites among these clusters was uneven. For instance, cluster #3 contained many sites ($n = 21$), whereas all the other clusters had fewer sites (#1: four sites, #2: five sites, #4: six sites, #5: four sites, #6 six sites). The parallel analysis with modified indices provided close classification results.

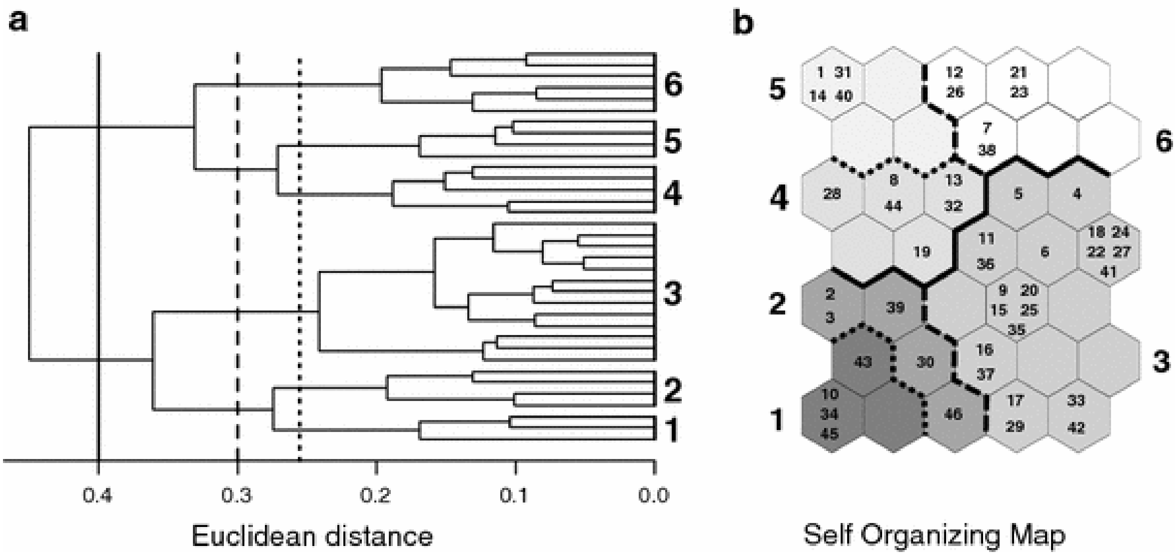


Fig. 2 Results of the SOM model. **a** Dendrogram showing the similarity between SOM output data and the cluster resulting from MRPP cutting strategy. **b** Distribution of sample sites on the SOM map using biodiversity and conservation indices. Cut-off levels are shown by vertical lines. Numbers in the map correspond to the site numbers and numbers outside the map correspond to the cluster numbers. In this map, waterbodies with similar basic conservation indices are presented either in the same output neuron, or in neighbouring ones

Conservation value patterns

The synthetic index, Q, was positively correlated to all the basic indices (Spearman correlation test with Holm-Bonferroni P-value correction, r between +0.50 and +0.76, $P < 0.05$ in all pairwise comparisons). The boxplot of Q (Fig. 3) also showed that the clustering method based on structure of the BBC, OI, RI and Rich indices discriminated well between sites with differing values of conservation interest (Kruskal–Wallis test, KW = 38.00, $P < 0.001$). In the six clusters, five different Q levels were significant (clusters #5 and #6 were not statistically different according to Dunn's post hoc test), 11 species displayed contrasting patterns in terms of their occurrence frequencies, and none was characteristic of a single cluster (Table 1). Overall, all the basic indices tended to decrease in line with the Q index gradient from cluster 1 to cluster 6 and showed few trend differences (Fig. 3). BCC index was separated into two levels, with the clusters #5 and #6 being the groups with the lowest values (Kruskal–Wallis test, KW = 20.50, $P < 0.001$; Dunn's post-hoc test). The OI index boxplot revealed significant differences between clusters (Kruskal–Wallis, KW = 24.73, $P < 0.001$; Dunn's post-hoc test), notably due to the low values of clusters #4 and #5. The values of the RI index were significantly higher for clusters #1 and #2, whereas the index values of the other clusters were below 0.4 (Kruskal–Wallis, KW = 22.32, $P < 0.001$; Dunn's post-hoc test). At last, the Rich index decreased gradually from cluster #1 to cluster #6 (Kruskal–Wallis, KW = 26.41, $P < 0.001$; Dunn's post-hoc test).

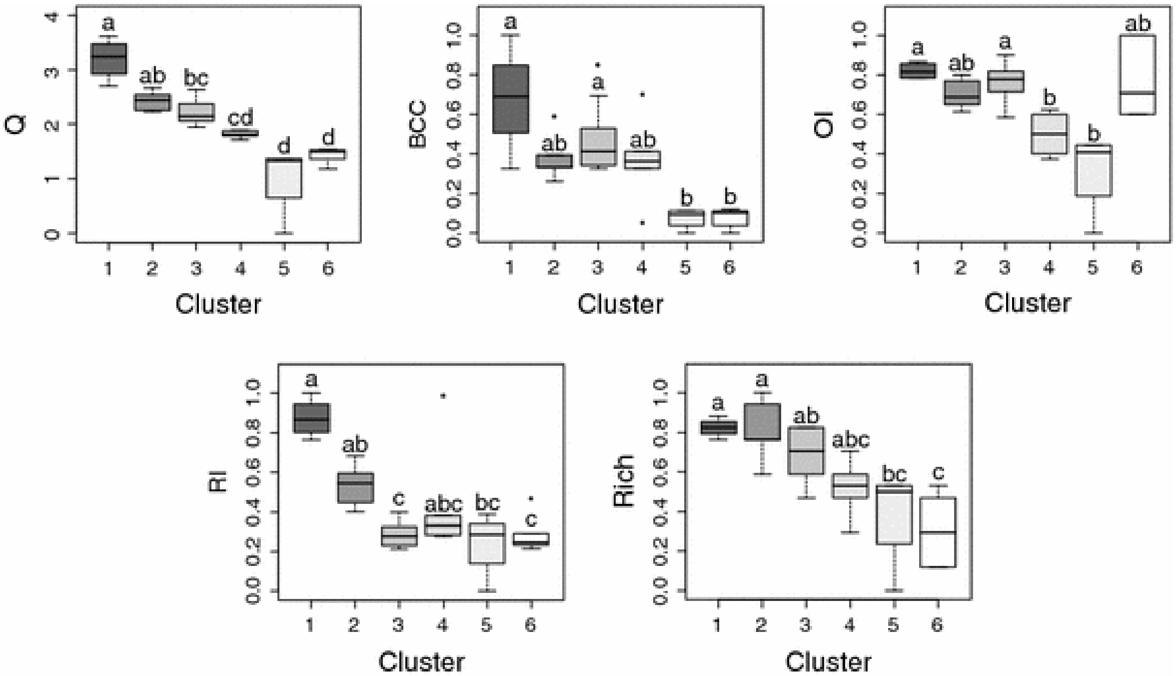


Fig. 3 Description of the classification obtained by SOM modelling. Box plots of *Q*, BCC, OI, RI and Rich values were plotted according to the clustering analysis, and organized along the MRPP homogeneity gradient. In each cluster, when Kruskall–Wallis tests were significant, Dunn's post-hoc tests were conducted (the same letter means that values were not statistically different)

Environmental determinism of conservation values

The MLP model explained a large part of the variance (Table 2). The connectivity and the percentage of floating aquatic vegetation had the greatest impact on the prediction of the *Q*, Rich and OI indices. The aquatic vegetation (floating and submerged) determined the BCC index prediction. Connectivity and topography were the most important variables for the RI index prediction. The sensitivity analysis and the Lowess smoothing curve indicated that connectivity exerted a positive influence on *Q*, OI, RI and Rich, all of which tended to increase, whereas aquatic vegetation had a negative impact on these indices, which tended to decrease (Fig. 4). The waterbodies with the highest values of RI had intermediate waterbed slope. The parallel analysis provided close predictions.

Table 2 Results of the MLP model

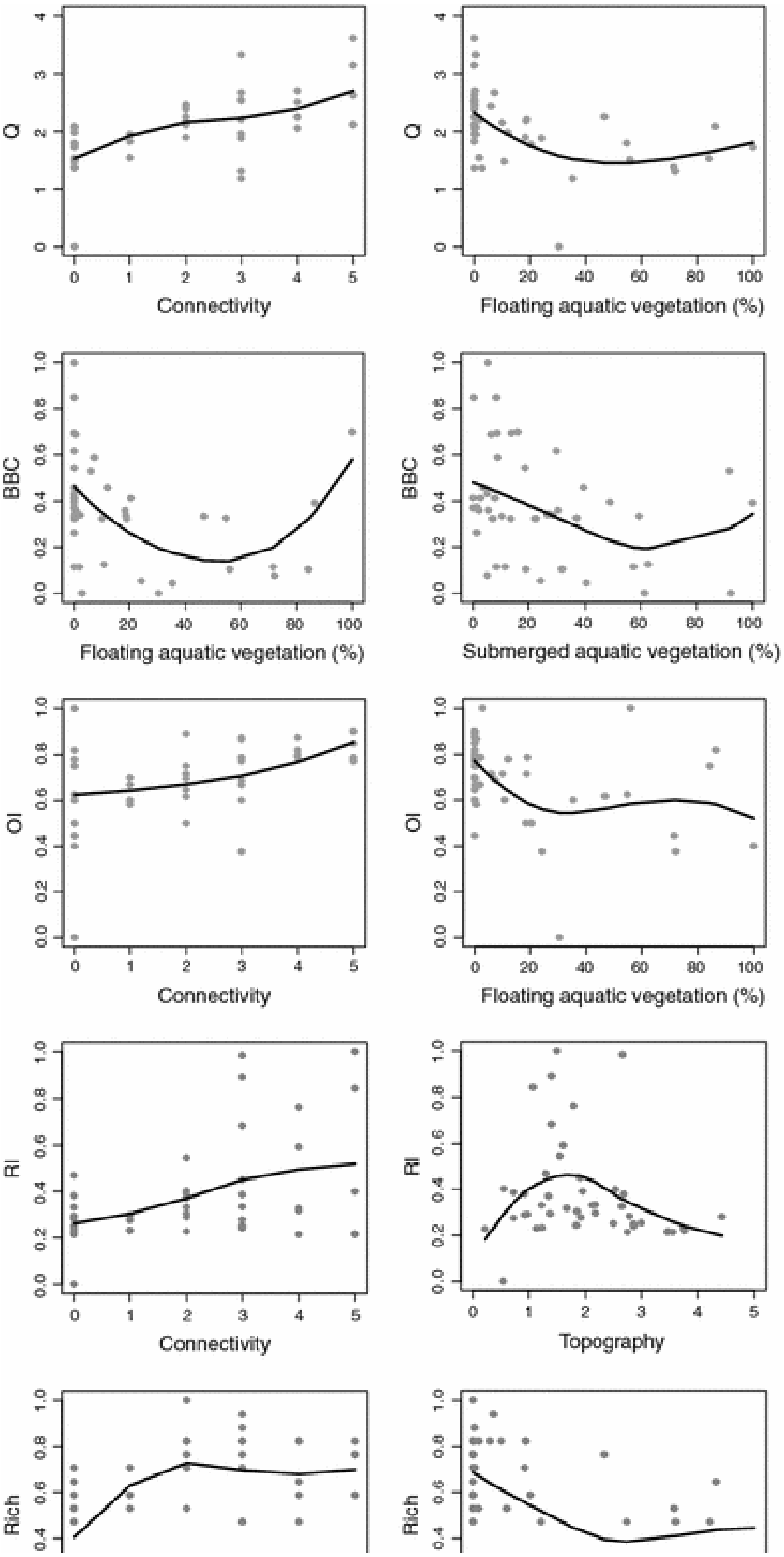
	Connectivity	Floating vegetation	Submerged vegetation	Topography	Pebbles	Silt	Distance to saline limit	R^2 a	Hidden neurons/ Iteration[b]
Q	+44 (8)	−44 (8)	4 (1)	6 (1)	0 (0)	0 (0)	1 (1)	0.85	8/180
BCC	6 (3)	−27 (6)	−27 (4)	20 (3)	2 (1)	8 (2)	10 (3)	0.94	8/160
OI	+28 (6)	−25 (7)	7 (4)	4 (2)	18 (4)	17 (4)	1 (1)	0.85	7/160
RI	+59 (6)	1(2)	1 (2)	−26 (1)	5 (2)	1 (1)	7 (3)	0.77	5/160

Rich	+19 (2)	−37 (4)	14 (1)	1 (0)	7 (2)	11 (3)	12 (1)	0.87	9/170

Relative contributions (SD) of the environmental variables from 50 MLP prediction models randomly initialised. For each index, the positive (+) and negative (−) effects of the most important factor on the prediction (in bold type) were obtained by the partial derivatives method

[a] R^2 represents the percentage of prediction of the model

[b]The hidden neurons/iteration correspond to the model parameters (see "Materials and methods")



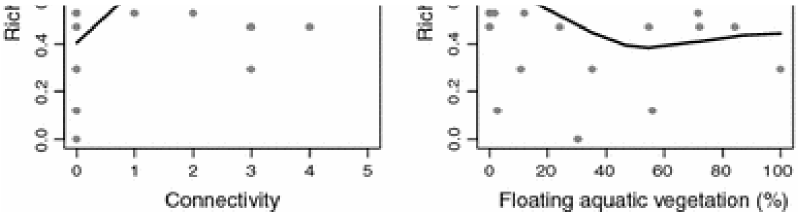


Fig. 4 Bivariate plots of Q, BCC, OI, RI and Rich values against the most important contributing variables in the ANN models. Solid lines indicate the Lowess curves used to fit the data

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Discussion

The heritage value of the Loire floodplain

Although our samplings had been done in the lentic bream zone (Lasne et al. 2007b), we caught some typical lotic fish characteristic of the barbel zone, such as the barbell (*Barbus barbus*), chub (*Leuciscus cephalus*) and dace (*Leuciscus leuciscus*). The diversity of these Loire waterbodies corresponded to approximately 40% of French fish species richness (Keith and Allardi 2001), and 90% of that of the Loire (Lasne et al. 2007b). The habitat heterogeneity of the floodplain (Lasne et al. 2007a) permits the co-occurrence of fish species, and means that the Loire floodplain can be classified as an area of major conservation interest at the scale of the Loire and the France as a whole.

BCC, OI, RI and Rich indices

The BCC is a basic index that uses several different endangerment criteria. For Fattorini (2006a), BCC is a sensitive index, particularly because it uses a definition of conservation status that is influenced by an update of the legal requirements. However, in our study we used an association of protection lists, and so the BCC index was not statistically significantly influenced by the number of lists used, and consequently less influenced by the updating of the regulations. Our study combined the IUCN status at the world scale with European lists of protected species (Habitat Directive and Berne Convention). In our dataset, only species with a LR status were existing in the IUCN list. In fact, we devised a no a priori calculation system, and it is proposed as a method potentially applicable to all freshwater fish communities as it does not depend on our dataset. Alternatively, a National Red List of freshwater fish (Keith and Marion 2002) could be used. However, including this list could lead to redundancy of information with that included in the Habitat Directive and the Berne Convention. In addition, it would be interesting to adapt the Red List methodology to the waterbody scale. Our findings showed that the BCC index values of the entire assemblage appeared to be negatively correlated to the abundance of aquatic vegetation. Among the six species with the highest conservation status (not strictly those included in the IUCN (LR), Table 1), five (the bleak *Alburnus alburnus*, the common nase *Chondrostoma nasus*, the spined loach *Cobitis taenia,* the barbell, *Barbus barbus* and the sea lamprey *Petromyzon marinus*) were rheophilic, and had no ideal habitat for their life cycle in the disconnected waterbodies, where vegetation abundance was high and there were no gravel banks suitable for breeding (Aarts and Nienhuis 2003). According to Aarts et al. (2004), species with conservation status can be viewed as being sensitive to environmental degradation. Consequently, the BCC index allows us to demonstrate that the degradation of waterbodies (the loss of clear water, increase in aquatic vegetation and eutrophication) has not been beneficial for species with high conservation status.

The proportions of native and non-native status of species also provide a good index of environment degradation (Clavero and Garciá-Berthou 2005). According to our findings, the most interesting waterbodies tend to have a high proportion of native species, and connectivity was the most important variable for this index. Although the aquatic habitats of floodplains provide attractive feeding and nursery environments (King et al. 2003), native fish tended to be more numerous and bigger in floodplains where there is good lateral connectivity (Jones and Stuart 2008). In fact, according to the review of Bunn and Arthington (2002), uniform flows resulting from river regulation can promote the local replacement of native species by non-native ones. The presence of aquatic vegetation also had a major impact on the OI index. The eutrophication of lake water leads to an increase in non-rooted macrophytes, and a reduction in rooted macrophytes (Hough et al. 1989). Thus, as non-native species are usually microhabitat generalists (Galat and Zweimüller 2001) that are able to benefit from environmental changes and survive in highly eutrophic sites (Copp et al. 2005), they will tend to replace native fish in eutrophic waterbodies with high aquatic vegetation. However, non-native species can be invasive, naturalized or introduced (Copp et al. 2005), and a Rich index weighted to allow for these different categories could be used to provide a better assessment of the degradation status of sites.

Kerr (1997) proposed a rarity index (which can also be considered to be an indicator of endemism) for large scale conservation planning. The application of the RI at the floodplain scale could lead to errors. For instance, a species found only once may indeed be a rare species, but could also be a species that is difficult to sample or an extra-zonal species accidentally present in the habitat investigated. However, the use of assemblages in our analyses allowed us to reduce the possible bias due to the inclusion of extra-zonal species. In our study, we considered as rare species that were found in only a few waterbodies (Cao et al. 2001) and rare fish communities or the high RIs that were consisted mainly of scarce species. Connectivity was the main predictor of the RI index at the floodplain scale; rarity being higher in connected waterbodies. This may have several causes. Firstly, connected habitats may be used by transient or foraging species from reaches further upstream or downstream (this is probably true in our study of the Atlantic flounder *Platichthys flesus,* which as found in most of the downstream connected waterbodies). Secondly, the lower rarity index in disconnected waterbodies may be due to the presence in these areas of generalist species, which may be also present in more connected habitats. Topography has much less impact on RI, but this impact is ambiguous. Finally, according to Santoul et al. (2005), it is very difficult to explain differences in the spatial rarity of species of freshwater habitats in terms of environmental variables.

Tockner et al. (1998) suggest that fish richness increases in floodplain waterbodies as lateral connectivity level increases. This was confirmed by our findings. However, in contrast to studies in tropical floodplains (Meschiatti et al. 2000; Petry et al. 2003), we found that aquatic vegetation cover had a negative impact on the species richness, possibly because the presence in temperate waterbodies of excessive aquatic vegetation leads to a fall in dissolved oxygen (Killgore and Hoover 2001). In addition, aquatic vegetation cover is often closely linked to connectivity levels, and can indeed be viewed as a covariable of connectivity (Lasne et al. 2007b).

Synthetic index *Q* as management tool

Though the basic indices were statistically independent, the positive correlation between the synthetic index *Q* with all of them demonstrated the power of *Q* to approximate the overall biodiversity and conservation value of the fish community in different waterbodies. Hence, the low scatter of *Q* values among groups identified by the clustering analysis showed the power of the statistical strategy used. The very high contribution of connectivity and floating aquatic vegetation to *Q* prediction (+44% and −44%, respectively) highlights the role of these variables in determining fish assemblage composition and structure, and hence the waterbody conservation value. Previous research has tended to highlight the role of hydrological connectivity on fish communities in floodplains (Amoros and Bornette 2002; Lasne et al. 2007a). Although the abundance of aquatic vegetation has usually been described as a consequence of waterbody connectivity (Bornette et al. 1998; Amoros and Bornette 2002), Petry et al. (2003) suggested that it might be important for fish distribution in tropical floodplains. In association with connectivity, our results also suggest that aquatic vegetation has a potential role in the conservation value of temperate waterbody territories. In the future, providing a functional study of the effects of aquatic vegetation on fish distribution in temperate waterbodies could be used to temper these results. The synthesis of information provided by the synthetic index *Q* and the fact that it can be rather accurately predicted by environmental variables makes it a powerful index of biodiversity value, and an interesting tool for guiding conservation and restoration management. In fact, at the scale of the Loire floodplain, our methodological process identified six statistically different clusters organized along a gradient of biodiversity and conservation value. Indeed, although the basic indices we used corresponded to fish community metrics, the fact we used no a priori discrimination method permitted us to propose a hierarchical classification of waterbodies that is independent of the composition of the fish communities. In addition, the clustering and prediction sensitivity tests realised with parallel analysis demonstrated the stability of the statistical strategy. Consequently, according to the definition of conservation value for our sites (i.e. sites with many species with conservation status, high richness, many rare species and few non-native species), the waterbodies belonging to cluster #1 are important sites for conservation. Conversely, waterbodies with few species, low conservation status, few rare species and a lot of non-native species included in clusters #5 and #6, require restoration management plans at least from a fish point of view. Consequently, according to our synthetic index (*Q*), the conservation of 4 waterbodies and restoration of 11 waterbodies (Fig. 1) the management program should integrate two important variables: connectivity and the associated spread of aquatic vegetation.

However, the prioritisation of sites, and the identification of important territories for biodiversity conservation or restoration should now involve a multi-taxa approach. Indeed, combining information about various different taxa is very informative for assessing the conservation value of a territory in a comprehensive manner and overlooking some taxa could well lead to a potential failure to protect freshwater biodiversity. Most conservation studies based on site prioritisation have been limited to a specific taxonomic group (Meijaard and Nijman *2003*; this study) or even to a species generally regarded as emblematic (Wei et al. *1999*). Although it is difficult to establish a conservation plan for species with differing preferences in terms of habitat (Carroll et al. *2001*), the integration of multi-taxa analyses could allow a more rigorous identification of areas of conservation interest. For example, if the conservation value of fish communities in a floodplain is strongly boosted by the connectivity that of amphibians is conversely higher in disconnected wetlands, such as ponds (Tockner et al. *1998*). Thus a multi-taxa approach would increase the relevance of conservation and restoration strategies and the management of freshwaters areas.

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